RAW SEQUENCE LISTING   DATE: 10/17/2001
PATENT APPLICATION: US/09/842,347   TIME: 14:55:22

Input Set : N:\Crf3\RULE60\09842347.txt
Output Set: N:\CRF3\10172001\I842347.raw

SEQUENCE LISTING
4 (1) GENERAL INFORMATION: **ENTERED**
6   (i) APPLICANT: TAKAHASHI, Tohru
7   SERIZAWA, Nobufusa
8   KOISHI, Ryuta
9   KAWASHIMA, Ichiro
11   (ii) TITLE OF INVENTION: EXPRESSION SYSTEMS UTILIZING
12   AUTOLYZING FUSION PROTEINS
13   AND A NOVEL REDUCING POLYPEPTIDE
15   (iii) NUMBER OF SEQUENCES: 19
17   (iv) CORRESPONDENCE ADDRESS:
18   (A) ADDRESSEE: Frishhauf, Holtz, Goodman, Langer & Chick, P.C.
19   (B) STREET: 767 Third Avenue-25th Floor
20   (C) CITY: New York
21   (D) STATE: New York
22   (E) COUNTRY: United States
23   (F) ZIP: 10017-2023
25   (v) COMPUTER READABLE FORM:
26   (A) MEDIUM TYPE: Floppy disk
27   (B) COMPUTER: IBM PC compatible
28   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29   (D) SOFTWARE: PatentIn Release #1.24
31   (vi) CURRENT APPLICATION DATA:
C--> 32   **(A) APPLICATION NUMBER: US/09/842,347**
C--> 33   **(B) FILING DATE: 25-Apr-2001**
34   (C) CLASSIFICATION:
44   (vii) PRIOR APPLICATION DATA:
37   (A) APPLICATION NUMBER: 09/167,151
38   (B) FILING DATE: 1998-10-06
41   (A) APPLICATION NUMBER: JP 6-218392
42   (B) FILING DATE: 13-SEP-1994
45   (A) APPLICATION NUMBER: JP 6-303809
46   (B) FILING DATE: 07-DEC-1994
48 (viii) ATTORNEY/AGENT INFORMATION:
49   (A) NAME: Goodman, Herbert
50   (B) REGISTRATION NUMBER: 17081
51   (C) REFERENCE/DOCKET NUMBER: 950376/HG
53   (ix) TELECOMMUNICATION INFORMATION:
54   (A) TELEPHONE: (212) 319-4900
55   (B) TELEFAX: (212) 319-5101
56   (C) TELEX: 236268
59 (2) INFORMATION FOR SEQ ID NO: 1:
61   (i) SEQUENCE CHARACTERISTICS:
62   (A) LENGTH: 1320 base pairs
63   (B) TYPE: nucleic acid
64   (C) STRANDEDNESS: double
65   (D) TOPOLOGY: linear

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```
      67      (ii) MOLECULE TYPE: cDNA to mRNA
W--> 69      (iii) HYPOTHETICAL: N
W--> 71       (iv) ANTI-SENSE: N
      73       (vi) ORIGINAL SOURCE:
      74           (A) ORGANISM: Clover Yellow Vein Virus
      76       (ix) FEATURE:
      77           (A) NAME/KEY: CDS
      78           (B) LOCATION: 1..1320
      79           (D) OTHER INFORMATION:
      80       (ix) FEATURE:
      81           (A) NAME/KEY: mat_peptide
      82           (B) LOCATION: 10..1311
      83           (D) OTHER INFORMATION:
      87       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
      89 AAG TTC CAA GGG AAA AGT AAG AGA ACA AGA CAA AAG TTG AAG TTC AGA      48
      90 Lys Phe Gln Gly Lys Ser Lys Arg Thr Arg Gln Lys Leu Lys Phe Arg
      91  1               5                   10                  15
      93 GCG GCA AGA GAC ATG AAG GAT CGT TAT GAA GTG CAT GCC GAT GAG GGG      96
      94 Ala Ala Arg Asp Met Lys Asp Arg Tyr Glu Val His Ala Asp Glu Gly
      95          20                  25                  30
      97 ACT TTA GTG GAA AAT TTT GGA ACT CGT TAT TCA AAG AAA GGC AAG ACA     144
      98 Thr Leu Val Glu Asn Phe Gly Thr Arg Tyr Ser Lys Lys Gly Lys Thr
      99          35                  40                  45
     101 AAA GGT ACT GTT GTG GGT TTG GGT GCA AAA ACA AGA CGG TTC ACT AAC     192
     102 Lys Gly Thr Val Val Gly Leu Gly Ala Lys Thr Arg Arg Phe Thr Asn
     103      50                  55                  60
     105 ATG TAT GGT TTT GAC CCC ACG GAG TAT TCA TTT GCT AGG TAT CTT GAT     240
     106 Met Tyr Gly Phe Asp Pro Thr Glu Tyr Ser Phe Ala Arg Tyr Leu Asp
     107  65                  70                  75                  80
     109 CCA ATC ACG GGT GCA ACA TTG GAT GAA ACC CCA ATT CAC AAT GTA AAT     288
     110 Pro Ile Thr Gly Ala Thr Leu Asp Glu Thr Pro Ile His Asn Val Asn
     111                  85                  90                  95
     113 TTG GTT GCT GAG CAT TTT GGC GAC ATA AGG CTT GAT ATG GTT GAC AAG     336
     114 Leu Val Ala Glu His Phe Gly Asp Ile Arg Leu Asp Met Val Asp Lys
W--> 115          100                 105                 110
     117 GAG TTA CTT GAC AAA CAG CAC TTA TAC CTC AAG AGA CCA ATA GAA TGT     384
     118 Glu Leu Leu Asp Lys Gln His Leu Tyr Leu Lys Arg Pro Ile Glu Cys
W--> 119          115                 120                 125
     121 TAC TTT GTA AAG GAT GCT GGT CAG AAG GTG ATG AGG ATT GAT CTA ACA     432
     122 Tyr Phe Val Lys Asp Ala Gly Gln Lys Val Met Arg Ile Asp Leu Thr
W--> 123          130                 135                 140
     125 CCC CAC AAC CCA TTG TTG GCA AGC GAT GTT AGC ACA ACC ATA ATG GGT     480
     126 Pro His Asn Pro Leu Leu Ala Ser Asp Val Ser Thr Thr Ile Met Gly
W--> 127 145                 150                 155                 160
     129 TAT CCT GAG AGA GAA GGT GAA CTC CGT CAA ACT GGA AAG GCA AGG TTA     528
     130 Tyr Pro Glu Arg Glu Gly Glu Leu Arg Gln Thr Gly Lys Ala Arg Leu
W--> 131              165                 170                 175
     133 GTC GAC CCA TCA GAG TTG CCC GCG CGG AAT GAG GAT ATT GAT GCA GAG     576
     134 Val Asp Pro Ser Glu Leu Pro Ala Arg Asn Glu Asp Ile Asp Ala Glu
```

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```
W--> 135             180                  185                  190
     137 TTT GAG AGT CTA AAT CGC ATA AGT GGT TTG CGC GAC TAT AAT CCC ATT      624
     138 Phe Glu Ser Leu Asn Arg Ile Ser Gly Leu Arg Asp Tyr Asn Pro Ile
W--> 139             195                  200                  205
     141 TCA CAA AAT GTT TGC TTG CTA ACA AAT GAG TCA GAA GGC CAT AGA GAG      672
     142 Ser Gln Asn Val Cys Leu Leu Thr Asn Glu Ser Glu Gly His Arg Glu
W--> 143     210                  215                  220
     145 AAG ATG TTT GGA ATT GGA TAT GGT TCA GTG ATC ATT ACA AAT CAA CAT      720
     146 Lys Met Phe Gly Ile Gly Tyr Gly Ser Val Ile Ile Thr Asn Gln His
W--> 147 225                  230                  235                  240
     149 CTG TTC AGA AGG AAT AAT GGG GAG TTA TCA ATT CAA TCC AAG CAT GGC      768
     150 Leu Phe Arg Arg Asn Asn Gly Glu Leu Ser Ile Gln Ser Lys His Gly
W--> 151             245                  250                  255
     153 TAC TTC AGA TGC CGC AAC ACC ACA AGC TTG AAG ATG CTG CCT TTG GAG      816
     154 Tyr Phe Arg Cys Arg Asn Thr Thr Ser Leu Lys Met Leu Pro Leu Glu
W--> 155             260                  265                  270
     157 GGA CAT GAC ATT TTG TTG ATT CAG TTA CCA AGG GAC TTT CCA GTG TTT      864
     158 Gly His Asp Ile Leu Leu Ile Gln Leu Pro Arg Asp Phe Pro Val Phe
W--> 159         275                  280                  285
     161 CCA CAA AAG ATT CGC TTT AGG GAG CCA AGA GTG GAT GAC AAA ATT GTT      912
     162 Pro Gln Lys Ile Arg Phe Arg Glu Pro Arg Val Asp Asp Lys Ile Val
W--> 163         290                  295                  300
     165 TTG GTC AGC ACA AAT TTC CAG GAA AAG AGT TCC TCG AGC ACG GTC TCA      960
     166 Leu Val Ser Thr Asn Phe Gln Glu Lys Ser Ser Ser Ser Thr Val Ser
W--> 167 305                  310                  315                  320
     169 GAG TCC AGT AAC ATT TCA AGA GTG CAG TCA GCC AAT TTC TAC AAG CAT     1008
     170 Glu Ser Ser Asn Ile Ser Arg Val Gln Ser Ala Asn Phe Tyr Lys His
W--> 171             325                  330                  335
     173 TGG ATC TCA ACA GTA GCA GGA CAC TGT GGA AAC CCT ATG GTT TCG ACT     1056
     174 Trp Ile Ser Thr Val Ala Gly His Cys Gly Asn Pro Met Val Ser Thr
W--> 175         340                  345                  350
     177 AAA GAT GGA TTT ATT GTA GGT ATC CAC AGT CTT GCT TCA TTG ACA GGC     1104
     178 Lys Asp Gly Phe Ile Val Gly Ile His Ser Leu Ala Ser Leu Thr Gly
W--> 179         355                  360                  365
     181 GAC GTT AAC ATC TTC ACA AGC TTT CCG CCG CAG TTT GAG AAC AAA TAT     1152
     182 Asp Val Asn Ile Phe Thr Ser Phe Pro Pro Gln Phe Glu Asn Lys Tyr
W--> 183     370                  375                  380
     185 CTA CAG AAG CTC AGT GAA CAC ACA TGG TGT AGT GGA TGG AAA CTA AAT     1200
     186 Leu Gln Lys Leu Ser Glu His Thr Trp Cys Ser Gly Trp Lys Leu Asn
W--> 187 385                  390                  395                  400
     189 CTT GGA AAG ATT AGT TGG GGT GGA ATC AAC ATT GTG GAG GAT GCA CCT     1248
     190 Leu Gly Lys Ile Ser Trp Gly Gly Ile Asn Ile Val Glu Asp Ala Pro
W--> 191             405                  410                  415
     193 GAA GAG CCC TTT ATA ACA TCC AAG ATG GCA AGC CTT CTT AGT GAT TTG     1296
     194 Glu Glu Pro Phe Ile Thr Ser Lys Met Ala Ser Leu Leu Ser Asp Leu
W--> 195             420                  425                  430
     197 AAT TGT TCA TTC CAA GCA AGT GCG                                     1320
     198 Asn Cys Ser Phe Gln Ala Ser Ala
W--> 199         435                  440
```

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Input Set : N:\Crf3\RULE60\09842347.txt
Output Set: N:\CRF3\10172001\I842347.raw

```
202 (2) INFORMATION FOR SEQ ID NO: 2:
204       (i) SEQUENCE CHARACTERISTICS:
205             (A) LENGTH: 440 amino acids
206             (B) TYPE: amino acid
207             (D) TOPOLOGY: linear
209       (ii) MOLECULE TYPE: protein
211       (vi) ORIGINAL SOURCE:
212             (A) ORGANISM: Clover Yellow Vein Virus
214       (ix) FEATURE:
215             (A) NAME/KEY: mat_peptide
216             (B) LOCATION: 4..437
217             (D) OTHER INFORMATION:
220       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
222 Lys Phe Gln Gly Lys Ser Lys Arg Thr Arg Gln Lys Leu Lys Phe Arg
223  1               5                  10                  15
225 Ala Ala Arg Asp Met Lys Asp Arg Tyr Glu Val His Ala Asp Glu Gly
226             20                  25                  30
228 Thr Leu Val Glu Asn Phe Gly Thr Arg Tyr Ser Lys Lys Gly Lys Thr
229             35                  40                  45
231 Lys Gly Thr Val Val Gly Leu Gly Ala Lys Thr Arg Arg Phe Thr Asn
232      50                  55                  60
234 Met Tyr Gly Phe Asp Pro Thr Glu Tyr Ser Phe Ala Arg Tyr Leu Asp
235  65                  70                  75                  80
237 Pro Ile Thr Gly Ala Thr Leu Asp Glu Thr Pro Ile His Asn Val Asn
238             85                  90                  95
240 Leu Val Ala Glu His Phe Gly Asp Ile Arg Leu Asp Met Val Asp Lys
241             100                 105                 110
243 Glu Leu Leu Asp Lys Gln His Leu Tyr Leu Lys Arg Pro Ile Glu Cys
244             115                 120                 125
246 Tyr Phe Val Lys Asp Ala Gly Gln Lys Val Met Arg Ile Asp Leu Thr
247      130                 135                 140
249 Pro His Asn Pro Leu Leu Ala Ser Asp Val Ser Thr Thr Ile Met Gly
250 145                 150                 155                 160
252 Tyr Pro Glu Arg Glu Gly Glu Leu Arg Gln Thr Gly Lys Ala Arg Leu
253             165                 170                 175
255 Val Asp Pro Ser Glu Leu Pro Ala Arg Asn Glu Asp Ile Asp Ala Glu
256             180                 185                 190
258 Phe Glu Ser Leu Asn Arg Ile Ser Gly Leu Arg Asp Tyr Asn Pro Ile
259             195                 200                 205
261 Ser Gln Asn Val Cys Leu Leu Thr Asn Glu Ser Glu Gly His Arg Glu
262      210                 215                 220
264 Lys Met Phe Gly Ile Gly Tyr Gly Ser Val Ile Ile Thr Asn Gln His
265 225                 230                 235                 240
267 Leu Phe Arg Arg Asn Asn Gly Glu Leu Ser Ile Gln Ser Lys His Gly
268             245                 250                 255
270 Tyr Phe Arg Cys Arg Asn Thr Thr Ser Leu Lys Met Leu Pro Leu Glu
271             260                 265                 270
273 Gly His Asp Ile Leu Leu Ile Gln Leu Pro Arg Asp Phe Pro Val Phe
274             275                 280                 285
```

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```
276  Pro Gln Lys Ile Arg Phe Arg Glu Pro Arg Val Asp Asp Lys Ile Val
277      290             295             300
279  Leu Val Ser Thr Asn Phe Gln Glu Lys Ser Ser Ser Ser Thr Val Ser
280  305             310             315             320
282  Glu Ser Ser Asn Ile Ser Arg Val Gln Ser Ala Asn Phe Tyr Lys His
283              325             330             335
285  Trp Ile Ser Thr Val Ala Gly His Cys Gly Asn Pro Met Val Ser Thr
286              340             345             350
288  Lys Asp Gly Phe Ile Val Gly Ile His Ser Leu Ala Ser Leu Thr Gly
289          355             360             365
291  Asp Val Asn Ile Phe Thr Ser Phe Pro Pro Gln Phe Glu Asn Lys Tyr
292      370             375             380
294  Leu Gln Lys Leu Ser Glu His Thr Trp Cys Ser Gly Trp Lys Leu Asn
295  385             390             395             400
297  Leu Gly Lys Ile Ser Trp Gly Gly Ile Asn Ile Val Glu Asp Ala Pro
298              405             410             415
300  Glu Glu Pro Phe Ile Thr Ser Lys Met Ala Ser Leu Leu Ser Asp Leu
301              420             425             430
303  Asn Cys Ser Phe Gln Ala Ser Ala
304          435             440
306  (2) INFORMATION FOR SEQ ID NO: 3:
308      (i) SEQUENCE CHARACTERISTICS:
309          (A) LENGTH: 25 base pairs
310          (B) TYPE: nucleic acid
311          (C) STRANDEDNESS: single
312          (D) TOPOLOGY: linear
314      (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
W-->316      (iii) HYPOTHETICAL: N
W-->318      (iv) ANTI-SENSE: N
322      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
324  GTCCATGGGG AAAAGTAAGA GAACA                                          25
326  (2) INFORMATION FOR SEQ ID NO: 4:
328      (i) SEQUENCE CHARACTERISTICS:
329          (A) LENGTH: 20 base pairs
330          (B) TYPE: nucleic acid
331          (C) STRANDEDNESS: single
332          (D) TOPOLOGY: linear
334      (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
W-->336      (iii) HYPOTHETICAL: N
W-->338      (iv) ANTI-SENSE: N
342      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
344  ACTCTGAGAC CGTGCTCGAG                                                20
346  (2) INFORMATION FOR SEQ ID NO: 5:
348      (i) SEQUENCE CHARACTERISTICS:
349          (A) LENGTH: 20 base pairs
350          (B) TYPE: nucleic acid
351          (C) STRANDEDNESS: single
352          (D) TOPOLOGY: linear
354      (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
```

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Input Set : N:\Crf3\RULE60\09842347.txt
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```
L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:69 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=1
L:71 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=1
L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:131 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:143 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:147 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:187 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:199 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:316 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=3
L:318 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=3
L:336 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=4
L:338 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=4
L:356 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=5
L:358 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=5
L:376 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=6
L:378 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=6
L:396 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=7
L:398 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=7
L:416 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=8
L:418 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=8
L:436 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=9
L:455 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=10
L:474 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=11
L:476 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=11
L:769 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=13
L:771 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=13
L:789 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=14
L:791 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=14
L:811 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=15
L:813 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=15
```

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Input Set : **N:\Crf3\RULE60\09842347.txt**
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```
L:831 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=16
L:833 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=16
L:851 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=17
L:853 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=17
L:871 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=18
L:873 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=18
L:894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
```